EXHIBIT B

EMBL-EBI

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ClustalW2 Results

Results of search	
Number of sequences	4
Alignment score	9231
Sequence format	Pearson
Sequence type	aa
JalView	Start JalView
Output file	clustalw2-20100803-1709277804.output
Alignment file	clustalw2-20100803-1709277804.aln
Guide tree file	clustalw2-20100803-1709277804.dnd
Your input file	clustalw2-20100803-1709277804.input

SUBMIT ANOTHER JOB

To save a result file right-click the file link in the above table and choose "Save Target As".
If you cannot see the JalView button, reload the page and check your browser settings to enable Java Applets.

Scores Table

Sort by   Sequence Number   View Output File

```
SeqA Name            Len(aa)  SeqB Name            Len(aa)  Score
======================================================================
1    Fischer_Phlp4>   10      2    SEQ#2>            500      30
1    Fischer_Phlp4>   10      3    SEQ#4>            500      30
1    Fischer_Phlp4>   10      4    SEQ#6>            500      30
2    SEQ#2>           500     3    SEQ#4>            500      99
2    SEQ#2>           500     4    SEQ#6>            500      92
3    SEQ#4>           500     4    SEQ#6>            500      92
======================================================================
```

PLEASE NOTE: Some scores may be missing from the above table if the alignment was done using multiple CPU mode. Please check the output.

Sort by   Sequence Number   View Output File

Alignment

Show Colors   View Alignment File

```
CLUSTAL 2.0.12 multiple sequence alignment


SEQ#2>          YFPPPAAKEDFLGCLVKEIPPRLLYAKSSPAYPSVLGQTIRNSRWSSPDNVKPIYIVTPT 60
SEQ#4>          YFPPPAAKEDFLGCLVKEIPPRLLYAKSSPAYPSVLGQTIRNSRWSSPDNVKPIYIVTPT 60
SEQ#6>          YFPPPAAKEDFLGCLVKEIPPRLLYAKSSPAYPSVLGQTIRNSRWSSPDNVKPLYIITPT 60
Fischer_Phlp4>  ------------------------------------------------------------


SEQ#2>          NASHIQSAVVCGRRHGVRIRVRSGGHDYEGLSYRSLQPEEFAVVDLSKMRAVWVDGKART 120
SEQ#4>          NASHIQSAVVCGRRHGVRIRVRSGGHDYEGLSYRSLQPEEFAVVDLSKMRAVWVDGKART 120
SEQ#6>          NVSHIQSAVVCGRRHSVRIRVRSGGHDYEGLSYRSLQPETFAVVDLNKMRAVWVDGKART 120
Fischer_Phlp4>  ------------------------------------------------------------


SEQ#2>          AWVDSGAQLGELYYAIHKASTVLAFPAGVCPTIGVGGNFAGGGFGMLLRKYGIAAENVID 180
SEQ#4>          AWVDSGAQLGELYYAIHKASPVLAFPAGVCPTIGVGGNFAGGGFGMLLRKYGIAAENVID 180
SEQ#6>          AWVDSGAQLGELYYAIYKASPTLAFPAGVCPTIGVGGNFAGGGFGMLLRKYGIAAENVID 180
Fischer_Phlp4>  --------------------IVALPX-------G----------MLK----------- 10
                                    :*:*        *          :*:


SEQ#2>          VKLVDANGTLHDKKSMGDDHFWAVRGGGGESFGIVVAWKVRLLPVPPTVTVFKIPKKASE 240
SEQ#4>          VKLVDANGTLHDKKSMGDDHFWAVRGGGGESFGIVVAWKVRLLPVPPTVTVFKIPKKASE 240
SEQ#6>          VKLVDANGKLHDKKSMGDDHFWAVRGGGGESFGIVVAWQVKLLPVPPTVTIFKISKTVSE 240
Fischer_Phlp4>  ------------------------------------------------------------


SEQ#2>          GAVDIINRWQVVAPQLPDDLMIRVIAQGPTATFEAMYLGTCQTLTPMMSSKFPELGMNAS 300
SEQ#4>          GAVDIINRWQVVAPQLPDDLMIRVIAQGPTATFEAMYLGTCQTLTPMMSSKFPELGMNAS 300
SEQ#6>          GAVDIINKWQVVAPQLPADLMIRIIAQGPKATFEAMYLGTCKTLTPLMSSKFPELGMNPS 300
Fischer_Phlp4>  ------------------------------------------------------------


SEQ#2>          HCNEMSWIQSIPFVHLGHRDNIEDDLLNRNNTFKPFAEYKSDYVYEPFPKRVWEQIFSTW 360
SEQ#4>          HCNEMSWIQSIPFVHLGHRDNIEDDLLNRNNTFKPFAEYKSDYVYEPFPKEVWEQIFSTW 360
SEQ#6>          HCNEMSWIQSIPFVHLGHRDALEDDLLNRNNSFKPFAEYKSDYVYQPFPKTVWEQILNTW 360
Fischer_Phlp4>  ------------------------------------------------------------


SEQ#2>          LLKPGAGIMIFDPYGATISATPEWATPFPHRKGVLFNIQYVNYWFAPGAGAAPLSWSKEI 420
```

```
SEQ#2>              YNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTFSSGLVWGQKYFKGNFQRLAITKGK  480
SEQ#4>              YNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTFSSGLVWGQKYFKGNFQRLAITKGK  480
SEQ#6>              YNYMEPYVSKNPRQAYANYRDIDLGRNEVVNDVSTYASGKVWGQKYFKGNFERLAITKGK  480
Fischer_Phlp4>      ------------------------------------------------------------


SEQ#2>              VDPTDYFRNEQSIPPLIKKY  500
SEQ#4>              VDPTDYFRNEQSIPPLIKKY  500
SEQ#6>              VDPTDYFRNEQSIPPLIKKY  500
Fischer_Phlp4>      --------------------
```

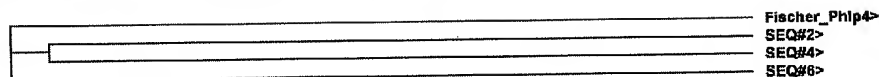*PLEASE NOTE: Showing colors on large alignments is slow.*

    Show Colors   View Alignment File

Guide Tree

    Show as Phylogram Tree   Show Distances   View DND File

```
(
Fischer_Phlp4>:0.66250,
(
SEQ#2>:0.00250,
SEQ#4>:0.00150)
:0.03550,
SEQ#6>:0.03750);
```

Cladogram

    Show as Phylogram Tree   Show Distances   View DND File

Right-click on the above tree to see display options.
Problems printing? Read how to print a Phylogram or Cladogram.